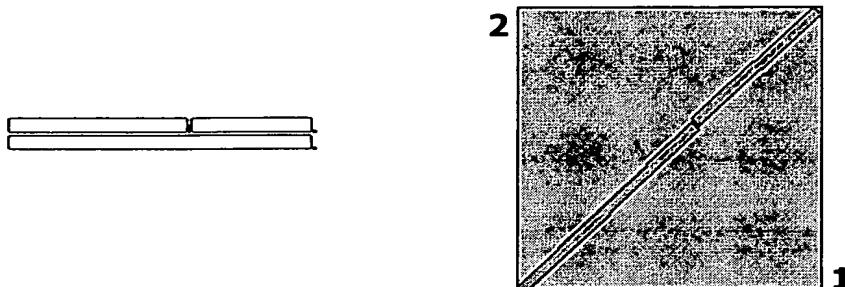


BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.5 [N v-16-2002]

Matrix **BLOSUM62** gap open:**11** gap extension:**1**
x_dropoff: **50** expect: **10.000** wordsize: **3** Filter Align

Sequence 1 |cl|seq_1 **Length** 101 (1 .. 101)

Sequence 2 |cl|seq_2 **Length** 102 (1 .. 102)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 147 bits (371), Expect = 4e -35
Identities = 61/101 (60%), Positives = 80 /101 (78%), Gaps = 1/101 (0%)

Query: 1 CKRHPLYVDFSDVGWNDWIVAPPGYHAFYC HGECPFPLADHLNSTNHAIQTLVNSVNSK 60
CK+H LYV F D+GW DWI+AP GY A+YC GEC FPL ++N+TNHAIQTLV+ +N +
Sbjct: 1 CKKHELYVSFRDLGWQDWIIAPEGYAAYYC EGECAFPLNSYMNATNHAIQTLVHFINPE 60

Query: 61 -IPKACCVPTELSAISMLYLDENEKVVLKNYQDMVVEGCGC 100
+PK CC PT+L+AIS+LY D++ V+LK Y++MVV CGC
Sbjct: 61 TVPKPCCAPTQLNAISVLYFDDSSNVILKK YRNMVVRACGC 101

CPU time: 0.03 user secs. 0.04 sys. secs 0.07 total secs.

Lambda K H
0.323 0.139 0.470

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 133
Number of Sequences: 0
Number of extensions: 3
Number of successful extensions: 2
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's successfully gapped in pr elim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non -prelim): 1
length of query: 101

length of database: 463,002,162
effective HSP length: 77
effective length of query: 24
effective length of database: 463,002,085
effective search space: 11112050040
effective search space used: 11112050040
T: 9
A: 40
X1: 16 (7.4 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.9 bits)
S2: 67 (30.4 bits)